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OCT 03 2003
FEDERAL TRADE COMMISSION

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,990A

DATE: 09/30/2003
TIME: 10:27:48

Input Set : E:\31276-20026.00 - seqlist (final) fixed.txt
Output Set: N:\CRF4\09302003\I759990A.raw

3 <110> APPLICANT: AntiCancer, Inc.
4 Xu, Mingxu
5 Han, Oinghong
7 <120> TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGH
8 SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLHOMOCYSTAINASE
9 (SAHH) AND IMPROVED ASSAYS FOR S-ADENOSYLMETHIONINE (SAM)
12 <130> FILE REFERENCE: 31276-20026.00
14 <140> CURRENT APPLICATION NUMBER: US 09/759,990A
15 <141> CURRENT FILING DATE: 2001-01-12
17 <150> PRIOR APPLICATION NUMBER: US 60/176,444
18 <151> PRIOR FILING DATE: 2000-01-14
20 <160> NUMBER OF SEQ ID NOS: 7
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1461
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens (nucleotide sequence of SAHH)
29 <400> SEQUENCE: 1

30	atggcttgc	aatcacccat	tgggtgc	tccatggat	acaatggcc	catcaaccc	60
31	catgttctcg	gcccgttgg	acttaccctt	gctggatgg	aaatggcc	aggctttttt	120
32	cttcgttgc	gttattccgc	ttctaa	gttgggtt	tcagaatctc	tggttccctc	180
33	cacatggat	tccagacac	cgatccatc	gagacactca	cagctttgg	tgctgtatgtc	240
34	agatgggctt	cctgttgc	acat	tttcttctaca	caagatata	ccgtgtgtc	300
35	ggcccaacag	gcacaccc	ggatggcc	gttata	ccatggcc	tcttcgttgc	360
36	acactccat	aatactgg	gaacacata	cgatccatc	catggcc	aggccatgg	420
37	ccacagcagg	ttgtcgat	ttgtgtgt	gttacactcc	tcatctccaa	gggtttcgaa	480
38	ttcgaaacag	ccgggtgt	tccagagcc	acagaagct	acaacccat	cgatccat	540
39	gttcttgc	tactcaag	ca	tttcaac	caagacaaga	accactgg	600
40	gccggcat	acgggtt	tttccatgg	cgaaagagaca	acaacagg	gttccatcc	660
41	gagaaggagg	gcaaaact	cttcc	cgcc	atcaacgt	gttccatcc	720
42	aagtgcata	acatctac	gg	ctgcgttcc	tcccttat	gttccatcc	780
43	gtatgtat	tcggcg	ccaa	gacagct	gttccat	ggcgatgt	840
44	tgcgttcaat	ccctccgt	gg	ccaggcg	gttccat	ccgtgttcc	900
45	tgcgttcc	aggctgc	cat	ggcttcc	gttccat	ccgtgttcc	960
46	gtatgtat	tcttcgtt	ac	atgcac	gttccat	ccgtgttcc	1020
47	gcccgat	aggataagg	tttgcgtt	acttgc	gttccat	ccgtgttcc	1080
48	acatggat	tcatgaaata	cccagg	cgatcc	caatca	aggccatcc	1140
49	atgtggat	tcccagat	gg	ccacgttac	tttgcgtt	ccgtgttcc	1200
50	cttggctgc	ctacagg	tttccat	gttgcgtt	tttgcgtt	ccgtgttcc	1260
51	ctcgctc	tcgac	tttccat	cgaaaagaga	ggaaatct	gttgcgtt	1320
52	ccgaaggat	tcgatgaa	gg	ccacgttac	tttgcgtt	ccgtgttcc	1380
53	acaaaagctt	cacagaag	gg	cttgcgttac	atcaacgtt	ccgtgttcc	1440
54	tctgtat	accgtt	tttccat	tttgcgtt	ccgtgttcc	ccgtgttcc	1461

ENTERED

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58 <210> SEQ ID NO: 2
59 <211> LENGTH: 33
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Upstream primer
66 <400> SEQUENCE: 2
67 ttttggatcc gcttgcaaat cacctgctgg tgc 33
70 <210> SEQ ID NO: 3
71 <211> LENGTH: 24
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Downstream primer
78 <400> SEQUENCE: 3
79 ttttctgcag ggggagctat cgct 24
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 38
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: Primer
89 <400> SEQUENCE: 4
90 catcatcatc atcatcacgc ttgcaaatca cctactgg 38
93 <210> SEQ ID NO: 5
94 <211> LENGTH: 30
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Primer
101 <400> SEQUENCE: 5
102 ctacgaatgg caataattcc taggtacgta 30
105 <210> SEQ ID NO: 6
106 <211> LENGTH: 1461
107 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens (nucleotide sequence of SAHH - wild type)
110 <400> SEQUENCE: 6
111 atggcttgc aatcacctgc tgggtctcca ttgcgagtaca gaattgccga catcaacctc 60
112 catgttctcg gccgtaagga acttaccctt gctgagaagg aatgccagg tcttatggtt 120
113 cttcgtgagc gttattccgc ttctaagcca ttgaagggtg tcagaatetc tggttccctc 180
114 cacatgacag tccagacagc ggtccttatt gagacactca cagctctgg tgctgatgtc 240
115 agatgggctt cctgcaacat ctctctaca caagatacag ccgctgctgc tattcgttg 300
116 ggcccaacag gcacaccaga gaagccagcc ggtatcccg tcttcgcctg gaagggcga 360
117 acactcccaag aatactggga gaacacatac cgcgctctca catggccaga tggtaaggc 420
118 ccacagcagg ttgtcgatga tgggtggat gctacactcc tcatactccaa gggcttcgaa 480
119 ttgcgaaacag ccgggtgtgt cccagagcca acagaagctg acaacctcga ataccgctgc 540
120 gttcttgcta cactcaagca ggttcaac caagacaaga accactggca cacagttgc 600
121 gccggcatga acggtgtttc cgaagagaca acaacaggtg tccaccgcct ctaccagctc 660
122 gagaaggagg gcaaactcct cttcccgagcc atcaacgtca acgacgctgt tacaaagtcc 720
  
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123	aagttcgata	acatctacgg	ctgtcgccac	tcccttacg	atggtatcaa	ccgtgcttcc	780											
124	gatgtcatga	tcggcggcaa	gacagctctc	gtcatgggt	acggcgatgt	cgggaagggc	840											
125	tgcgctcaat	ccctccgtgg	ccaaggcgct	cgcgttatca	tcacagaact	cgaccctata	900											
126	tgcgctctcc	aggctgtcat	ggaaggctac	caggtccgcc	gcatcgagga	agtctgtcaag	960											
127	gatgtcgata	tcttcgttac	atgcacagga	aactgcgata	tcatctctgt	tgacatgtat	1020											
128	gcccgatgt	aggataaggc	tattgtcggt	aacatcgccc	acttcgataa	cgaatttgat	1080											
129	acagatggcc	tcatgaaata	cccaggcatc	aagcacatcc	caatcaagcc	agaatacgac	1140											
130	atgtggaaat	tcccagatgg	ccacgctatc	ctcccttcttg	ctgagggccg	ccttcttaac	1200											
131	cttgggttgcg	ctacaggctca	cccatcttcc	gttatgtcaa	tgtcattcac	aaaccagaca	1260											
132	ctcgctcagc	tcgacccctca	cgaaaagaga	ggaaatctcg	agatgaaggt	ttacacactt	1320											
133	ccgaagcattc	tcgatgaaga	agtcgttcgc	ctccacctcg	gatctctcg	tgtccacctt	1380											
134	acaaagctta	cacagaagca	ggctgactac	atcaacgttc	cagttgaggg	tccttacaag	1440											
135	tctgtatgtt	accgttatta	a				1461											
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139	<211>	LENGTH:	486															
140	<212>	TYPE:	PRT															
141	<213>	ORGANISM:	Homo sapiens															
143	<400>	SEQUENCE:	7															
144	Met	Ala	Cys	Lys	Ser	Pro	Thr	Gly	Ala	Pro	Phe	Glu	Tyr	Arg	Ile	Ala		
145	1						5			10					15			
146	Asp	Ile	Asn	Leu	His	Val	Leu	Gly	Arg	Lys	Glu	Leu	Thr	Leu	Ala	Glu		
147							20			25				30				
148	Lys	Glu	Met	Pro	Gly	Leu	Met	Val	Leu	Arg	Glu	Arg	Tyr	Ser	Ala	Ser		
149							35			40				45				
150	Lys	Pro	Leu	Lys	Gly	Val	Arg	Ile	Ser	Gly	Ser	Leu	His	Met	Thr	Val		
151							50			55				60				
152	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala	Leu	Gly	Ala	Asp	Val		
153							65			70				75			80	
154	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln	Asp	Thr	Ala	Ala	Ala		
155							85			90				95				
156	Ala	Ile	Val	Val	Gly	Pro	Thr	Gly	Thr	Pro	Glu	Lys	Pro	Ala	Gly	Ile		
157							100			105				110				
158	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Thr	Leu	Pro	Glu	Tyr	Trp	Glu	Asn		
159							115			120				125				
160	Thr	Tyr	Arg	Ala	Leu	Thr	Trp	Pro	Asp	Gly	Gln	Gly	Pro	Gln	Gln	Val		
161							130			135				140				
162	Val	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Leu	Leu	Ile	Ser	Lys	Gly	Phe	Glu		
163							145			150				155			160	
164	Phe	Glu	Thr	Ala	Gly	Ala	Val	Pro	Glu	Pro	Thr	Glu	Ala	Asp	Asn	Leu		
165							165			170				175				
166	Glu	Tyr	Arg	Cys	Val	Leu	Ala	Thr	Leu	Lys	Gln	Val	Phe	Asn	Gln	Asp		
167							180			185				190				
168	Lys	Asn	His	Trp	His	Thr	Val	Ala	Ala	Gly	Met	Asn	Gly	Val	Ser	Glu		
169							195			200				205				
170	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	Gln	Leu	Glu	Lys	Glu	Gly		
171							210			215				220				
172	Lys	Leu	Leu	Phe	Pro	Ala	Ile	Asn	Val	Asn	Asp	Ala	Val	Thr	Lys	Ser		
173							225			230				235			240	
174	Lys	Phe	Asp	Asn	Ile	Tyr	Gly	Cys	Arg	His	Ser	Leu	Ile	Asp	Gly	Ile		

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175	245	250	255						
176	Asn Arg Ala Ser Asp Val Met Ile Gly Gly Lys Thr Ala Leu Val Met								
177	260	265	270						
178	Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Gln Ser Leu Arg Gly Gln								
179	275	280	285						
180	Gly Ala Arg Val Ile Ile Thr Glu Leu Asp Pro Ile Cys Ala Leu Gln								
181	290	295	300						
182	Ala Ala Met Glu Gly Tyr Gln Val Arg Arg Ile Glu Glu Val Val Lys								
183	305	310	315						
184	320	325	330						
185	Asp Val Asp Ile Phe Val Thr Cys Thr Gly Asn Cys Asp Ile Ile Ser								
186	335	340	345						
187	Val Asp Met Met Ala Gln Met Lys Asp Lys Ala Ile Val Gly Asn Ile								
188	350	355	360						
189	365	370	375						
190	Gly Ile Lys His Ile Pro Ile Lys Pro Glu Tyr Asp Met Trp Glu Phe								
191	380	385	390						
192	400	405	410						
193	Pro Asp Gly His Ala Ile Leu Leu Leu Ala Glu Gly Arg Leu Leu Asn								
194	415	420	425						
195	Leu Gly Cys Ala Thr Gly His Pro Ser Phe Val Met Ser Met Ser Phe								
196	430	435	440						
197	445	450	455						
198	Leu Glu Lys Lys Val Tyr Thr Leu Pro Lys His Leu Asp Glu Glu Val								
199	460	465	470						
200	201	202	203	204	205	Ala Arg Leu His Leu Gly Ser Leu Asp Val His Leu Thr Lys Leu Thr	Gln Lys Gln Ala Asp Tyr Ile Asn Val Pro Val Glu Gly Pro Tyr Lys	Ser Asp Ala Tyr Arg Tyr	480
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VERIFICATION SUMMARY

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DATE: 09/30/2003

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Input Set : E:\31276-20026.00 - seqlist (final) fixed.txt
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